

1 ATGCTGTTCCGCGCCGGGGCCGGTACGGGCAGGGCTGGGGCGCCGGAGGCT 60  
 1 M L F R A R G P V R G R G W G R P A E A 20  
  
 61 CCCCGCCGCGGGCGCTCGCCGCCCTGGAGCCCCGCTGGATTGCTGCTGGCGCTGCC 120  
 21 P R R G R S P P W S P A W I C C W A L A 40  
  
 121 GGCTGCCAGGGCCCTGGCTGGGACCTGCCCTCCAGCCGCCGCTCCCT 180  
 41 G C Q A A W A G D L P S S S S R P L P P 60  
  
 181 TGCCAGGAGAAAGATTATCACTTGAATATAAGGAATGTGATAGCAGTGGCTCCAGGTGG 240  
 61 C Q E K D Y H E E Y T E C D S S S G S R W 80  
  
 241 AGAGTTGCCATTCAAATTCTGCAGTGGACTGCTCTGGCTGCCAGCCAGTGAGAGGC 300  
 81 R V A I P N S A V D C S G L P D P V R G 100  
  
 301 AAAGAATGCACTTCTCCTGTGCTCTGGAGAGTATCTAGAAATGAAGAACAGGTATGC 360  
 101 K E C T F S C A S G E Y L E M K N Q V C 120  
  
 361 AGTAAGTGGTGAAGGCACCTATTCTGGCAGTGGCATCAAATTGATGAATGGAT 420  
 121 S K C G E G T Y S L G S G I K F D E W D 140  
  
 421 GAATTGCCGGCAGGATTTCTAACATCGAACATTGACACTGTGGTGGCCCTCT 480  
 141 E L P A G F S N I A T F M D T V V G P S 160  
  
 481 GACAGCAGGCCAGACGGCTGTAACAACCTTCTGGATCCCTCGGAAACTACATAGAA 540  
 161 D S R P D G C N N S S W I P R G N Y I E 180  
  
 541 TCTAATCGTGTGACTGCACGGTGTCTTGATCTATGCTGTGCACCTTAAGAAGTCAGGC 600  
 181 S N R D D C T V S L I Y A V H L K K S G 200  
  
 601 TATGTCTTGTGAGTACCAAGTATGTCGACAACAACATCTTCTTGAGTTCTTATTCAA 660  
 201 Y V F F E Y Q Y V D N N I F F E F F I Q 220

## FIG. 1A



661 AATGATCAGTGCCAGGAGATGGACACCACACTGACAAGTGGTAAAACCTACAGACAAT 720  
 221 N D Q C Q E M D T T T D K W V K L T D N 240  
  
 721 GGAGAATGGGGCTCTCATTCTGTAATGCTGAAATCAGGCACAAACATACTCTACTGGACA 780  
 241 G E W G S H S V M L K S G T N I L Y W R 260  
  
 781 ACTACAGGCATCCTTATGGTTCTAAGGCGGTCAAGCCCTGTGCTGGTAAAAAATACACA 840  
 261 T T G I L M G S K A V K P V L V K N I T 280  
  
 841 ATTGAAGGGTGGCGTACACATCAGAATGTTTCTTCAAGGCCAGGCACATTCAAGCAAC 900  
 281 I E G V A Y T S E C F P C K P G T F S N 300  
  
 901 AAACCAGGTTCAATTCAACTGCCAGGTGTCCCAGAAACACCTATTCTGAGAAAGGAGCC 960  
 301 K P G S F N C Q V C P R N T Y S E K G A 320  
  
 961 AAAGAATGTATAAGGTGAAAGACGACTCTCAATTTCAGGATCCAGTGACTGTACAGAG 1020  
 321 K E C I R C K D D S Q F S G S S E C T E 340  
  
 1021 CGCCCTCCCTGTACCAACAAAGACTATTCCAGATCCATACTCCATGTGATGAAGAAGGA 1080  
 341 R P P C T T K D Y F Q I H T P C D E E G 360  
  
 1081 AAGACACAGATAATGTACAAGTGGATAGGCCAAAATCTGCCGGAGGATCTCACAGAT 1140  
 361 K T Q I M Y K W I E P K I C R E D L T D 380  
  
 1141 GCTATTAGATTGCCCTCTGGAGAGAAGAAGGATTGTCCGCCTGCAACCCCTGGATT 1200  
 381 A I R L P P S G E K K D C P P C N P G F 400  
  
 1201 TATAACAATGGATCATCTTCTTGCATCCCTGTCTCTGGAACATTTCAGATGGAACC 1260  
 401 Y N N G S S S C H P C P P G T F S D G T 420  
  
 1261 AAAGAATGTAGACCATGTCCAGCAGGAACGGAGGCCTGCACTTGGCTTGAAATAAATGG 1320  
 421 K E C R P C P A G T E P A L G F E Y K W 440

## FIG. 1B



1321 TGGAAATGTCCTCCTGGCAACATGAAAACCTCCTGCTCAATGTTGGAAATTCAAAGTGC 1380  
 441 W N V L P G N M K T S C F N V G N S K C 460  
  
 1381 GATGGAATGAATGGTTGGGAGGTGGCTGGAGATCATATCCAGAGTGGGCTGGAGGTTCT 1440  
 461 D G M N G W E V A G D H I Q S G A G G S 480  
  
 1441 GACAATGATTACCTGATCTTAACTTGCATATCCCAGGATTAAACCAACATCTATG 1500  
 481 D N D Y L I L N L H I P G F K P P T S M 500  
  
 1501 ACTGGAGCCACGGGTCTGAACTAGGAAGAATAACATTGTCTTGAGACCCCTGTCA 1560  
 501 T G A T G S E L G R I T F V F E T L C S 520  
  
 1561 GCTGACTGTGTTTGACTTCATGGTGGATTTAATAGAAAAAGTACAAATGTGGTAGAA 1620  
 521 A D C V L Y F M V D I N R K S T N V V E 540  
  
 1621 TCGTGGGTGGAACCAAGAAAAACAAGCTTACACCCATATCATCTCAAGAATGCACT 1680  
 541 S W G G T K E K Q A Y T H I I F K N A T 560  
  
 1681 TTTACATTTACATGGCATTCCAGAGAACTAATCAGGGTCAAGATAATAGACGGTCATC 1740  
 561 F T F T W A F Q R T N Q G Q D N R R F I 580  
  
 1741 AATGACATGGTGAAGATTTATTCTATCACAGCCACTAATGCCATTGATGGGTGGCCT 1800  
 581 N D M V K I Y S I T A T N A V D G V A S 600  
  
 1801 TCATGCCGTGCCCTGTGCCCTCGGTTCTGAACAGTCGGTTCATCGTGTCCCCTGCCCT 1860  
 601 S C R A C A L G S E Q S G S S C V P C P 620  
  
 1861 CCAGGCCACTACATTGAGAAAGAAACCAACCAAGTGCAGGAATGTCACCTGACACCTAC 1920  
 621 P G H Y I E K E T N Q C K E C P P D T Y 640  
  
 1921 CTGTCCATACATCAGGTCTATGGCAAAGAGGCTTGTATTCCATGGGGCTGGAGTAAA 1980  
 641 L S I H Q V Y G K E A C I P C G P G S K 660

## FIG. 1C



1981 AACAAATCAGGACCATTGGTTGCTATAGTGACTGCTTTCTACCATGAAAAGAAAAT 2040  
 661 N N Q D H S V C Y S D C F F Y H E K E N 680  
  
 2041 CACATTTGCACTATGACTTTAGCAACCTCAGCAGTGTGGGCTATTAATGAATGGCCC 2100  
 681 Q I L H Y D F S N L S S V G S L M N G P 700  
  
 2101 AGCTTCACCTCAAAGGAACAAATACTTCATTTCTCAATATCAGTTATGTGGCAT 2160  
 701 S F T S K G T K Y F H F F N I S L C G H 720  
  
 2161 GAGGGAAAGAAGATGGCTCTGTACCAACAATATAACAGACTTACAGTAAAGAAATA 2220  
 721 E G K K M A L C T N N I T D F T V K E I 740  
  
 2221 GTGGCAGGGTCAGATGATTACACAAATTGGTAGGGCATTGTATGCCAGTCACAAATT 2280  
 741 V A G S D D Y T N L V G A F V C Q S T I 760  
  
 2281 ATTCCCTCTGAAACTAAGGGTTCCGAGCAGCCTTATCATCACAAATCCATCATTCTGGCA 2340  
 761 I P S E S K G F R A A L S S Q S I I L A 780  
  
 2341 GATACATTCAAGGAGTCACAGTTGAAACACATTGAAAATATTAAATATAAAAGAAGAT 2400  
 781 D T F I G V T V E T T L K N I N I K E D 800  
  
 2401 ATGTTCCCAGTTCCAACAAGCAAATACCAAGATGTGCAATTCTTTATAAGTCTCTACA 2460  
 801 M F P V P T S Q I P D V H F F Y K S S T 820  
  
 2461 GCAACAACATTTGTATTAATGGCCGATCAACTGCTGTGAAAATGAGGTGTAATCCTACT 2520  
 821 A T T S C I N G R S T A V K M R C N P T 840  
  
 2521 AAATCTGGAGCAGGAGTCATTCACTCCCCAGCAAGTGGCCAGCAGGTACCTGTGATGGG 2580  
 841 K S G A G V I S V P S K C P A G T C D G 860  
  
 2581 TGTACGTTCTATTCCTGTGGGAGAGTGCTGAAGCTGCCCTGTGTACGGAGCATGAC 2640  
 861 C T F Y F L W E S A E A C P L C T E H D 880

## FIG. 1D



2641	TTCCATGAGATTGAGGGAGCCTGCAAGAGAGGATTCAGGAAACCTGTATGTGTGGAAT	2700
881	F H E I E G A C K R G F Q E T L Y V W N	900
2701	GAACCTAAATGGTCATTAAAGGATTCTTGCCTGAGAAAAAGTTGGCAACCTGTGAA	2760
901	E P K W C I K G I S L P E K K L A T C E	920
2761	ACGGTTGACTTTGGCTGAAGGTGGAGCCGGTGTGGAGCTTTACTGCCGTTTGCTG	2820
921	T V D F W L K V G A G V G A F T A V L L	940
2821	GTGGCTCTGACCTGCTACTTCTGAAAAAGAATCAAAAGAAAAAGACCATTGAAAT	2880
941	V A L T C Y F W K K N Q K K K K T I L N	960
2881	CTGTTCAACTGAAAACCTCAAGATCCCCAAATATATGAAGAGACAGTGCTGTAGCCTG	2940
961	L F N *	964
2941	GACTAATGAACAAAGAAACCTGCTCTAGTTTACAGGACCATATTTAGGGTCTGCTC	3000
3001	ATACCTGTCACATTGGTGATCTCACAGAGGAGGCCATGCCGTGAAAGGAAAGGAGAT	3060
3061	TGAAACATTGATTGCCTTATCACATGGTCAAGTACCTGCCAAATAAGGAAAGCAAAT	3120
3121	GATTGGGTCTCACTGAAGATGAAGCTCAACTCAGGAAGAGATTATCTGTATATAACAC	3180
3181	ATAACTGAAAACCAAGTTAAGCCCACCAATGCCACTGCTGATGCCATATAATTAAAT	3240
3241	GGGTAACTTTATTCTTATGATGTCTACATAACAAGTGTGATTGGAAGGCACATGTGA	3300
3301	GCATATGCATTATGATCCAATTATGTTTTCTTGTATATTGGGAAAATTAAA	3360
3361	ATTTTTTAAGTAAAAAAAAAAAAAA	3390

FIG. 1E



## FIG. 2A

			10	20	30	
1	MLPRA RGPVR G R G W G R B A E A P R R G R S P P W S	TR16.aa				
1	----- D I K N L - L T V -----	EMB	CAB41042.1 TNFR			
1	----- C V G A R R L G R G P -----	emb	CAA53576.1 OX40			
			40	50	60	
31	PAWICCCWALAGCQAAWAGDPLESSSSRBLPE	TR16.aa				
10	----- C T I F Y I T T L A T A D -----	EMB	CAB41042.1 TNFR			
13	----- C A A L L L L G L G L S T -----	emb	CAA53576.1 OX40			
			70	80	90	
61	C Q E K D Y H F E Y T E C D S S G S R W R V A I P N S A V D	TR16.aa				
23	----- I P T S S L P -----	EMB	CAB41042.1 TNFR			
26	----- V - - T G L H -----	emb	CAA53576.1 OX40			
			100	110	120	
91	C S G L E D P E V R G K E C T F S C A S G E Y L E M K N Q V C	TR16.aa				
30	----- H A E V N G -----	EMB	CAB41042.1 TNFR			
31	----- A C D E G E V L D K R H N Q C -----	emb	CAA53576.1 OX40			
			130	140	150	
121	S K C G E G T Y S L G S G I K F D E W D E L P A G E S N I A	TR16.aa				
51	-----	EMB	CAB41042.1 TNFR			
43	-----	emb	CAA53576.1 OX40			
			160	170	180	
151	T F M D T V V G P S D S R P D G C N N S S W I P R G N Y I E	TR16.aa				
51	-----	EMB	CAB41042.1 TNFR			
43	-----	emb	CAA53576.1 OX40			
			190	200	210	
181	S N R D D C T V S L I Y A V H L K K S G Y V F F E Y O Y V D	TR16.aa				
51	-----	EMB	CAB41042.1 TNFR			
43	-----	emb	CAA53576.1 OX40			
			220	230	240	
211	N N I F F E F I O N D O C O E M D T T D K W V K L T D N	TR16.aa				
51	-----	EMB	CAB41042.1 TNFR			
43	-----	emb	CAA53576.1 OX40			
			250	260	270	
241	G E W G S H S V M L K S G T N I L Y W R T T G I L M G S K A	TR16.aa				
51	-----	EMB	CAB41042.1 TNFR			
43	-----	emb	CAA53576.1 OX40			
			280	290	300	
271	V K P V L V K N I T I E G V A Y T S E C F E C K P G T F S N	TR16.aa				
51	----- C N Q C C B P G E F A K -----	EMB	CAB41042.1 TNFR			
43	----- C H E C R E G N G M V -----	emb	CAA53576.1 OX40			
			310	320	330	
301	K P G S F N C O V C P R N T M Y S E K G A K E C I R C K D D S	TR16.aa				
62	----- V R C N -----	EMB	CAB41042.1 TNFR			
54	----- S R C S -----	emb	CAA53576.1 OX40			



## FIG. 2B

331	Q F S G S S E C T E R R E P C T T K D Y F Q I R T F C D E E G	TR16.aa
66	- - - - -	EMB   CAB41042.1 TNFR
58	- - - - -	emb   CAA53576.1 OX40
361	K T Q I M Y K W I E P K I C R E D L T D A I R L P P S G E K	TR16.aa
66	- - - - -	G N D N EMB   CAB41042.1 TNFR
58	- - - - -	R S Q N emb   CAA53576.1 OX40
391	K D C F F B C N P G E Y N N E G S S S C H P C P P G T F S D G T	TR16.aa
70	T K C E R C P E H T Y T A I P N Y S N G C - - - - -	EMB   CAB41042.1 TNFR
62	T V C R F C G P G F Y N D V V S - S K P C - - - - -	emb   CAA53576.1 OX40
421	K E C R P C P A G T E P A L G F E Y K W W N V L P G N M K T	TR16.aa
91	H Q C R K C - - P T G S - - - - -	F D K V EMB   CAB41042.1 TNFR
82	K P G T W C N L R S G S - - - - -	E R K Q emb   CAA53576.1 OX40
451	S C F N V G N S K C D G M N G W E V A G D H I Q S G A G G S	TR16.aa
105	K C T G T Q N S K C S C L P G W Y C A T D S S O T - - - - -	EMB   CAB41042.1 TNFR
98	L C T A T Q D T V C R C R A G - - - T Q P L D S - - - - -	emb   CAA53576.1 OX40
481	D N D Y L I L N L H I P G F K P P T S M T G A T G S E L G R	TR16.aa
130	- - - - - E D - - - - -	EMB   CAB41042.1 TNFR
119	- - - - - Y K P - - - - -	emb   CAA53576.1 OX40
511	I T F V F E T L C S A D C V L Y F M V D I N R K S T N V V E	TR16.aa
132	- - - - - C R A D C I - - - - -	EMB   CAB41042.1 TNFR
122	- - - - - G V D C A - - - - -	emb   CAA53576.1 OX40
541	S W G G T K E K O A Y T H I I F K N A T F T F T W A F Q R T	TR16.aa
137	- - - - -	EMB   CAB41042.1 TNFR
127	- - - - -	emb   CAA53576.1 OX40
571	N O G O D N R R F I N D M V K I Y S I T A T N A V D G V A S	TR16.aa
137	- - - - - P K R R - - - - -	EMB   CAB41042.1 TNFR
127	- - - - - P - - - - -	emb   CAA53576.1 OX40
601	S C R A C A L G S E O S G S S C V P C P P G H Y I E K E T N	TR16.aa
141	- - - - - C P C G Y F - - - - -	EMB   CAB41042.1 TNFR
128	- - - - - C P P G H F - - - - -	emb   CAA53576.1 OX40

FIG. 2C

640	650	660	
631 <b>Q C K E C C P P D T Y L S I P H Q V Y G K E A C I P C G P G S K</b>			TR16.aa
147 - - - - -			GGI EMB   CAB41042.1 TNFR
134 - - - - -			SPG emb   CAA53576.1 OX40
670 680 690			
661 <b>N N Q D H S V C Y S D C F F V H E K E N Q I L H Y D F S N L</b>			TR16.aa
150 D E Q G N P I C			EMB   CAB41042.1 TNFR
137 D N Q A - - C			emb   CAA53576.1 OX40
700 710 720			
691 <b>S S V G S L M N G P S F T S K G T K Y F H F F N I S L C G H</b>			TR16.aa
158 - - - - - K S			CCV EMB   CAB41042.1 TNFR
142 - - - - - K P W T N			CTL emb   CAA53576.1 OX40
730 740 750			
721 <b>E G K K M A L C T N N I T D F T V K E I V A G S D D Y T N L</b>			TR16.aa
163 G E - - - - -			EMB   CAB41042.1 TNFR
150 A G K H - - - - -			emb   CAA53576.1 OX40
760 770 780			
751 <b>V G A F V C Q S T I I P S E S K G F R A A L S S O S I I L A</b>			TR16.aa
166 - - - - - C D			EMB   CAB41042.1 TNFR
166 - - - - - C E D R D P P A T Q P Q E T Q G P P A R P I T V Q			emb   CAA53576.1 OX40
790 800 810			
781 <b>D T F I G V T V E T T E K N I N I K E D M F F P V P T S O I P</b>			TR16.aa
168 - - - - -			EMB   CAB41042.1 TNFR
191 P T - - - - -			emb   CAA53576.1 OX40
820 830 840			
811 <b>D V H F F Y K S S T A T T S C I N G R S T A V K M R C N P T</b>			TR16.aa
168 - - - - -			EMB   CAB41042.1 TNFR
203 - - - - - S T R P V E V P G G R A V A A I L - - - - -			emb   CAA53576.1 OX40
850 860 870			
841 <b>K S G A G V I S V P S K C P A G T C D G C T F Y F L W E S A</b>			TR16.aa
168 - - - - -			EMB   CAB41042.1 TNFR
220 - - G L G L V - - - - -			emb   CAA53576.1 OX40
880 890 900			
871 <b>E A C P L C T E H D F H E I E G A C K T G F O E T L Y V W N</b>			TR16.aa
168 - - - - -			Y L - - EMB   CAB41042.1 TNFR
229 - - G P L - - - - -			A I L L A L Y L L R emb   CAA53576.1 OX40
910 920 930			
901 <b>E P K W C I R G I S L H E K K L A T C E T V D F W L K V G A</b>			TR16.aa
170 - - - - - R N Y R L D P - - - - -			EMB   CAB41042.1 TNFR
242 - - - - - R D Q R L E P D A H K P - - - - -			P emb   CAA53576.1 OX40



## FIG. 2D

940 950 960

931 **G V G A E T A V I L V A L T C Y F W K K N Q K K K K T I L N** TR16.aa  
 177 **----- E -----** PPPKLS EMB | CAB41042.1 TNFR  
 255 **G G G S E R T P I ----- Q E E Q A D A H S T H A** emb | CAA53576.1 OX40

961 **L F N**  
 184 K C - N  
 276 K I

TR16.aa  
 EMB | CAB41042.1 TNFR  
 emb | CAA53576.1 OX40

TR16.aa



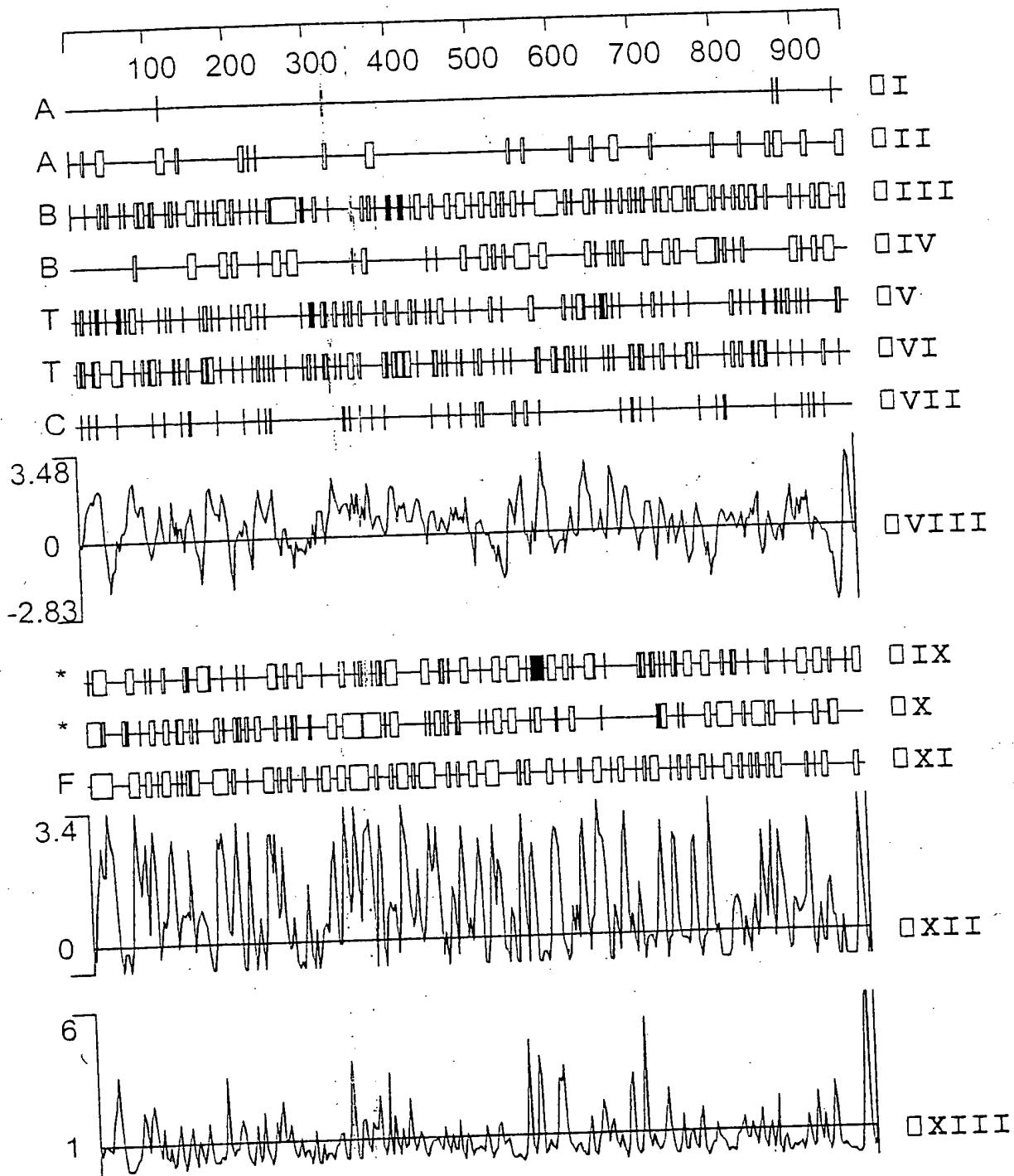


FIG. 3

1 ATGCTGTTCCGGCCCCGGGGCGGTACGGGCAGGGCTGGGGCGCCGGAGGCT 60  
 1 M L F R A R G P V R G R G W G R P A E A 20  
  
 61 CCCCGCCGGCCGCTGCCGCGCTGGAGCCCGCTGGATTCGCTGGCGCTGCC 120  
 21 P R R G R S P P W S P A W I C C W A L A 40  
  
 121 GGCTGCCAGGGCGCTGGGCTGGGACCTGCCCTCTCCAGCCGGCTTCCTCCT 180  
 41 G C Q A A W A G D L P S S S S R P L P P 60  
  
 181 TGCCAGGAGAAAGATTATCACTTGAATATACGGAATGTGATAGCACTGGCTCCAGGTGG 240  
 61 C Q E K D Y H F E Y T E C D S S S G S R W 80  
  
 241 AGAGTTGCCATTCAAATTCTGCACTGGACTGCTCTGCCCTGCCAGTGAAGAGGC 300  
 81 R V A I P N S A V D C S G L P D P V R G 100  
  
 301 AAAGAATGCACTTCTCCTGTGCTCTGGAGAGTATCTAGAAATGAAGAACCAAGGTATGC 360  
 101 K E C T F S C A S G E Y L E M K N Q V C 120  
  
 361 AGTAAGTGTGAAGGCACCTATTCTGGGACTGGCATCAAATTGATGAATGGGAT 420  
 121 S K C G E G T Y S L G S G I K F D E W D 140  
  
 421 GAATTGCCGGCAGGATTTCTAACATCGAACATTGACACTGTGGTGGCCCTCT 480  
 141 E L P A G F S N I A T F M D T V V G P S 160  
  
 481 GACAGCAGGCCAGACGGCTGTAACAACCTTCTGGATCCCTCGTGGAAACTACATAGAA 540  
 161 D S R P D G C N N S S W I P R G N Y I E 180  
  
 541 TCTAACGTGATGACTGCCGGTGTCTTGATCTATGCTGTGCACCTTAAGAAGTCAGGC 600  
 181 S N R D D C T V S L I Y A V H L K K S G 200  
  
 601 TATGTCTTCTTGAGTACCAAGTATGTCGACAACAACATCTTCTTGAGTTCTTATTCAA 660  
 201 Y V F F E Y Q Y V D N N I F F E F F I Q 220  
  
 661 AATGATCACTGCCAGGAGATGGACACCAACTGACAAGTCGGTAAAACCTACAGACAAT 720  
 221 N D Q C Q E M D T T D K W V K L T D N 240

FIG. 4A



721	GGAGAATGGGGCTCTCATTCTGTAATGCTGAAATCAGGCACAAACATACTCTACTGGAGA	780
241	G E W G S H S V M L K S G T N I L Y W R	260
781	ACTACAGGCATCCTTATGGGTTCTAAGGCGCTAAGCCTGTGCTGGTAAAAAATATCACA	840
261	T T G I L M G S K A V K P V L V K N I T	280
841	ATTGAAGGGTGGCGTACACATCAGAAATGTTTCCTTGCAGGCCAGGCACATTCAAGAAC	900
281	I E G V A Y T S E C F P C K P G T F S N	300
901	AAACCAGGTTCACTCAACTGCCAGGTGTGCTCCAGAAACACCTATTGTGAGAAAGGAGCC	960
301	K P G S F N C Q V C P R N T Y S E K G A	320
961	AAAGAATGTATAAGGTGTAAAGACGACTCTCAATTTCAGGATCCAGTGAGTGTACAGAG	1020
321	K E C I R C K D D S Q F S G S S E C T E	340
1021	CGCCCTCCCTGTACCAAAAGACTATTCCAGATCCATACTCCATGTGATGAAGAAGGA	1080
341	R P P C T T K D Y F Q I H T P C D E E G	360
1081	AAGACACAGATAATGTACAAGTGGATAGAGCCAAAATCTGCCGGAGGATCTCACAGAT	1140
361	K T Q I M Y K W I E P K I C R E D L T D	380
1141	GCTATTAGATTGCCCTCTGGAGAGAAGGATTGTCCGCCTGCAACCTGGATT	1200
381	A I R L P P S G E K K D C P P C N P G F	400
1201	TATAACAATGGATCATCTCTGCCATCCCTGTCCCTGGAACATTTAGATGGAACC	1260
401	Y N N G S S S C H P C P P G T F S D G T	420
1261	AAAGAATGTAGACCATGTCCAGCAGGAACGGAGCCTGCACTGGCTTGAATATAATGG	1320
421	K E C R P C P A G T E P A L G F E Y K W	440
1321	TGGAATGTCCCTCTGGCAACATGAAAACCTCCTGCTCAATGTTGGATTCAAAGTGC	1380
441	W N V L P G N M K T S C F N V G N S K C	460
1381	GATGGAATGAATGGTGGAGGTGGCTGGAGATCATATCCAGAGTGGGGCTGGAGGTTCT	1440
461	D G M N G W E V A G D H I Q S G A G G S	480

FIG. 4B



1441 GACAATGATTACCTGATCTTAAACTTGCATATCCCAGGATTTAACCAACATCTATG 1500  
 481 D N D Y L I L N L H I P G F K P P T S M 500  
  
 1501 ACTGGAGCCACGGGTTCTGAAGTAGGAAGAATAACATTGTCTTGAGACCCCTCTGTTCA 1560  
 501 T G A T G S E L G R I T F V F E T L C S 520  
  
 1561 GCTGACTGTGTTTGTACTTCATGGTGGATATTAATAGAAAAAGTACAAATGTGGTAGAA 1620  
 521 A D C V L Y F M V D I N R K S T N V V E 540  
  
 1621 TCGTGGGTGGAACCAAGAAAAACAAGCTTACACCCATATCATCTCAAGAATGCAACT 1680  
 541 S W G G T K E K Q A Y T H I I F K N A T 560  
  
 1681 TTTACATTTACATGGGCATTCCAGAGAACTAATCAGGTCAAGATAATAGACGGTCATC 1740  
 561 F T F T W A F Q R T N Q G Q D N R R F I 580  
  
 1741 AATGACATGGTGAAGATTATTCTATCACAGCCACTAATGCCAGTTGATGGGTGGCGTCC 1800  
 581 N D M V K I Y S I T A T N A V D G V A S 600  
  
 1801 TCATGCCGTGCTGTGCCCTCGTTCTGAACACTCGGGTTCATGTGTGTCCCTGCCCT 1860  
 601 S C R A C A L G S E Q S G S S C V P C P 620  
  
 1861 CCAGGCCACTACATTGAGAAAGAAACCAACCAAGTGCAGGAATGTCCACCTGACACCTAC 1920  
 621 P G H Y I E K E T N Q C K E C P P D T Y 640  
  
 1921 CTGTCCATACATCAGGTCTATGGAAAGAGGCTTGTATTCCATGGGGCTGGGACTAAA 1980  
 641 L S I H Q V Y G K E A C I P C G P G S K 660  
  
 1981 ACAATCAGGACCATTGGTTTGCTATAGTGAATGCTTTCTACCATGAAAAAGAAAAT 2040  
 661 N N Q D H S V C Y S D C F F Y H E K E N 680  
  
 2041 CAGATTTGCACTATGACTTTAGCAACCTCAGCAGTGTGGGCTATTAATGAATGGCCCC 2100  
 681 Q I L H Y D F S N L S S V G S L M N G P 700  
  
 2101 AGCTTCACCTCAAAGGAACAAAATACTTCCATTCTTCATATCAGTTATGTGGGCAT 2160  
 701 S F T S K G T K Y F H F F N I S L C G H 720

FIG. 4C



2161	GAGGGAAAGATGGCTCTGTACCAACAATATAACAGACTTACAGTAAAGAAATA	2220
721	E G K K M A L C T N N I T D E T V K E I	740
2221	GTGCCAGGGTCAGATGATTACACAAATTGGTAGGGCATTGTATGCCAGTCACAAATT	2280
741	V A G S D D Y T N L V G A F V C Q S T I	760
2281	ATTCCTCTGAAAGTAAGGTTCCGAGCAGCCTTATCATCACAAATCCATCATTCTGGCA	2340
761	I P S E S K G F R A A L S S Q S I I L A	780
2341	GATACATTCAAGGAGTCACAGTGAACACATTGAAAAATATTAATATAAAAGAAGAT	2400
781	D T F I G V T V E T T L K N I N I K E D	800
2401	ATGTTCCCAGTCCAACAAGC <sub>AA</sub> ATACCAAGATGTGATTTCTTTATAAGTCTTCTACA	2460
801	M F P V P T S Q I P D V H F F Y K S S T	820
2461	GCAACAAACATCTGTATTAATEGCCGATCAACTGCTGTGAAATGAGGTGTAATCCTACT	2520
821	A T T S C I N G R S T A V K M R C N P T	840
2521	AAATCTGGAGCAGGAGTGATTCAGTCCCCAGCAAGTGCCAGCAGGTACCTGTGATGGG	2580
841	K S G A G V I S V P S K C P A G T C D G	860
2581	TGTACGTTCTATTCCTGTGGAGAGTGTGAAGCTGCCCTGTGTACGGAGCATGAC	2640
861	C T F Y F L W E S A E A C P L C T E H D	880
2641	TTCCATGAGATTGAGGGAGCTGCAAGAGAGGATTCAAGGAAACCTGTATGTGGAAT	2700
881	F H E I E G A C K R G F Q E T L Y V W N	900
2701	GAACCTAAATGGTCATTAAGGAATTCTTGCCTGAGAAAAAGTGGCAACCTGTGAA	2760
901	E P K W C I K G I S L P E K K L A T C E	920
2761	ACGGTTGACTTTGGCTGAAGGTGGAGCCGGTGTGGAGCTTTACTGCCGTTTGCTG	2820
921	T V D F W L K V G A G V G A F T A V L L	940
2821	GTGGCTCTGACCTGCTACTCTGAAAAAGATCAAAACTGGAATACAAATATTCCAAG	2880
941	V A L T C Y F W K K N Q K L E Y K Y S K	960

FIG. 4D



2881 TTAGTAATGACGACTAACTCAAAAGAGTGTGAACCTCCGGCTGCAGACAGTTGTGCTATC 2940  
 961 L V M T T N S K E C E L P A A D S C A I 980  
  
 2941 ATGGAAGGAGAAAGATAATGAAGAGGAAGTTGTATATTCCAATAAACAGTCACTACTAGGA 3000  
 981 M E G E D N E S E V V Y S N K Q S L L G 1000  
  
 3001 AAACTCAAATCTTGGCAACCAAGGAAAAAGAACCTTTGAATCTGTTCAACTGAAA 3060  
 1001 K L K S L A T K E K E D H F E S V Q L K 1020  
  
 3061 ACCTCAAGATCCCCAATATAATGAAGAGACAGTGCTGTAGCCTTGAGACTAATGAACAAA 3120  
 1021 T S R S P N I 1028  
  
 3121 GAAACCTGCTCTAGTTTACAGGACCATAAGGCTGCTGCTCCTCATACCTGTACATT 3180  
  
 3181 GGTGATCTCACAGAGGAGGGCCATGCCGCTGAAAAGGGAGGAGATTGAAACATTGATT 3240  
  
 3241 GCCTTATCACATGGTCAAGTACCTGCCAATAAGGAAAGCAAATGATTGGCTCTCAA 3300  
  
 3301 CTGAAGATGAAGCTCAACTCAGGAAGAGATTATCTGTATATACACATAACTGAAAACCA 3360  
  
 3361 AGTTTAAGCCCACCAATGCACTGCTGTGATGCCATATAATTAAATGGTAACCTTTATT 3420  
  
 3421 CTTTATGATGCTACATAACAAGTGTGATTGGAAGGCACATGTGAGCATATGCATTATG 3480  
  
 3481 ATCCAATTATGTTTTCTTGTATATTGGGAAAATTAAATTAAAGGTA 3540  
  
 3541 AAAAAAAAAAAAAAA 3556

## FIG. 4E



10073333.081902

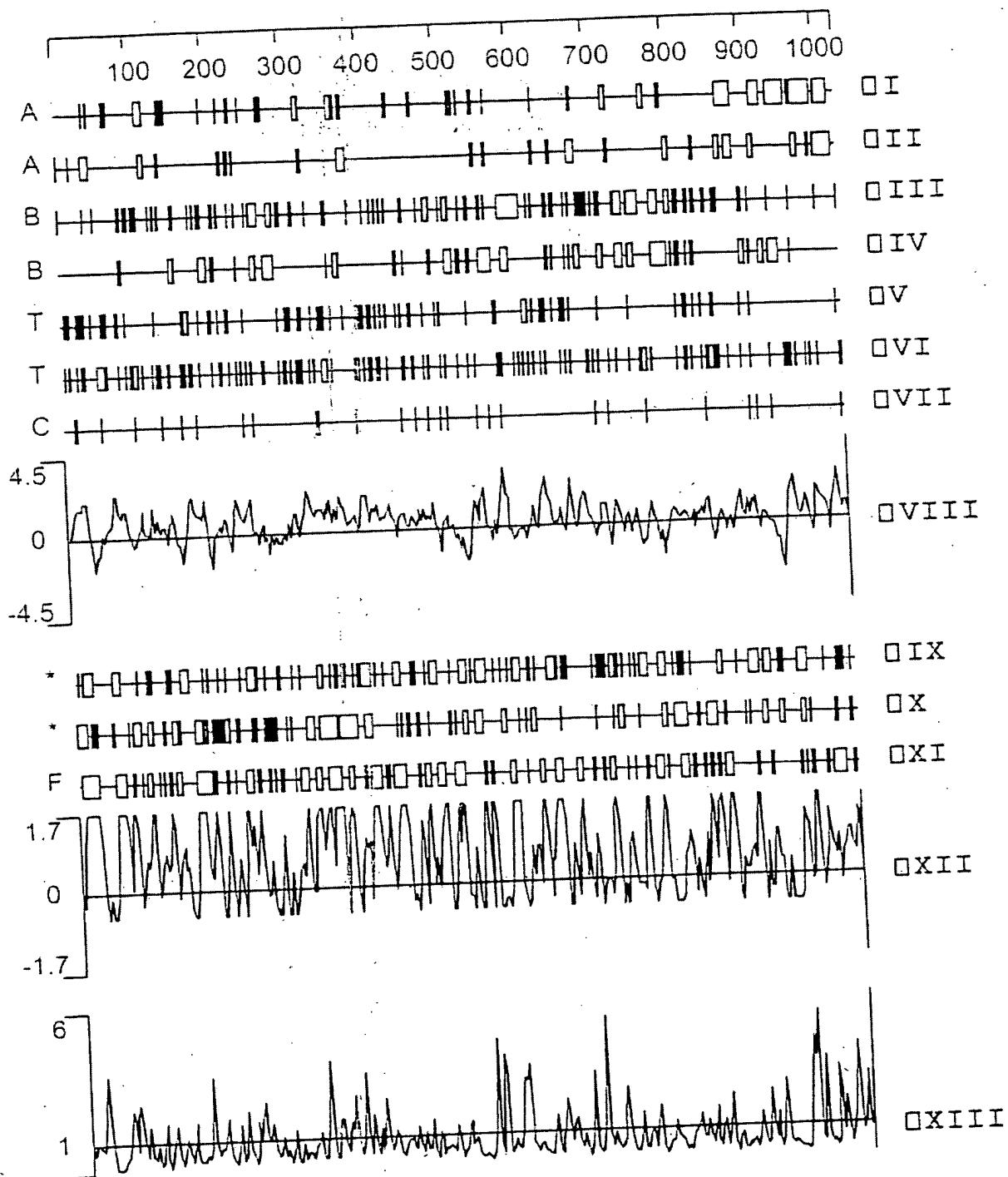


FIG. 5

O I P E JC176  
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	10	20	30	40	
1	M E F R A R G P V R G R G W G R P A E A P R R G R S P P W S P A W I C C W A L A				SEQ ID 2 SEC10
1	-----	-----	-----	-----	
	50	60	70	80	
41	G C Q A A W A G D L P S S S S R P L P P C Q E K D Y H F E Y T E C D S S G S R W				SEQ ID 2 SEC10
1	-----	-----	-----	-----	
	90	100	110	120	
81	R V A I P N S A V D C S G L P D P V R G K E C T F S C A S G E Y L E M K N Q V C				SEQ ID 2 SEC10
1	-----	-----	-----	-----	
	130	140	150	160	
121	S K C G E G T Y S L G S G I K P D E W D E L P A G E S N I A T E M D T V V G P S				SEQ ID 2 SEC10
7	S K C G E G T Y S L G S G I K P D E W D E L P A G E S N I A T E M D T V V G P S				
	170	180	190	200	
161	D S R P D G C N N S S W I P R G N Y I E S N R D D C T V S L I Y A V H L K K S G				SEQ ID 2 SEC10
47	D S R P D G C N N S S W I P R G N Y I E S N R D D C T V S L I Y A V H L K K S G				
	210	220	230	240	
201	Y V F F E Y Q Y V D N N I F F E F F I Q N D Q C Q E M D T T T D K W V K L T D N				SEQ ID 2 SEC10
87	Y V F F E Y Q Y V D N N I F F E F F I Q N D Q C Q E M D T T T D K W V K L T D N				
	250	260	270	280	
241	G E W G S H S V M L K S G T N I L Y W R T T G I L M G S K A V K R P V L V K N I T				SEQ ID 2 SEC10
127	G E W G S H S V M L K S G T N I L Y W R T T G I L M G S K A V K R P V L V K N I T				
	290	300	310	320	
281	I E G V A Y T S E C E P C K P G T F S N K P G S F N C Q V C P R N T Y S E K G A				SEQ ID 2 SEC10
167	I E G V A Y T S E C E P C K P G T F S N K P G S F N C Q V C P R N T Y S E K G A				
	330	340	350	360	
321	K E C I R C K D D S Q F S - G S S E C T E R P P C T T K D Y F Q I H T P C D E				SEQ ID 2 SEC10
207	K E C I R C K D D S Q F S E E G S S E C T E R P P C T T K D Y F Q I H T P C D E				
	370	380	390	400	
359	E G K T Q I M Y K W I E P K I C R E D L T D A I R L P P S G E K K D C P P C N P				SEQ ID 2 SEC10
247	E G K T Q I M Y K W I E P K I C R E D L T D A I R L P P S G E K K D C P P C N P				
	410	420	430	440	
399	G F Y N N G S S S C H P C P F G T F S D G T K E C R P C P A G T E P A L G F E Y				SEQ ID 2 SEC10
287	G F Y N N G S S S C H P C P F G T F S D G T K E C R P C P A G T E P A L G F E Y				
	450	460	470	480	
439	K W W N V L P G N M K T S C F N V G N S K C D G M N G W E V A G D H I Q S G A G				SEQ ID 2 SEC10
327	K W W N V L P G N M K T S C F N V G N S K C D G M N G W E V A G D H I Q S G A G				
	490	500	510	520	
479	G S D N D Y L I L N L H I P G F K P F T S M T G A T G S E L G R I T F V E F T L				SEQ ID 2 SEC10
367	G S D N D Y L I L N L H I P G F K P F T S M T G A T G S E L G R I T F V E F T L				

FIG. 6A



530 540 550 560  
 519 **CSADC**CVLYFMVDINRKSTNVVVE SWGGTKEKQAYTHIEKN SEQ ID 2  
 407 **CSADC**CVLYFMVDINRKSTNVVVE SWGGTKEKQAYTHIEKN SEC10

570 580 590 600  
 559 **ATFTETW**AFQRTNQGQDNRRFINDMVKIYSITATNAVDGV SEQ ID 2  
 447 **ATFTETW**GIPRE----- SEC10

610 620 630 640  
 599 **A**SSCRACALGSEQSGSSCVPCPPGHYIEKETNQCKECPPD SEQ ID 2  
 459 ----- SEC10

650 660 670 680  
 639 TYLSIHQVYGKEACIPCGPGSKNNQDHSVCYSDCFFYHEK SEQ ID 2  
 459 ----- SEC10

690 700 710 720  
 679 ENQILHYDFSNLSSVGSLMNGESFTSKGTKYFHFFNISLC SEQ ID 2  
 459 ----- LIQGER SEC10

730 740 750 760  
 719 GHEGKKMALCTNNITDFTVKEIVAGSDDYTNLVGAFVCQS SEQ ID 2  
 464 ----- SEC10

770 780 790 800  
 759 TIIIPSESKGFRAALSSQSIILADTFIGVTVETTLKNINIK SEQ ID 2  
 464 ----- SEC10

810 820 830 840  
 799 EDMFPVPTSQIPDVHFFYKSSTATTSCINGRSTAVKMRCN SEQ ID 2  
 464 ----- SEC10

850 860 870 880  
 839 PTKSGAGVVISVPSKCPAGTCDGCTFYFLWESAEACPLCTE SEQ ID 2  
 464 ----- SEC10

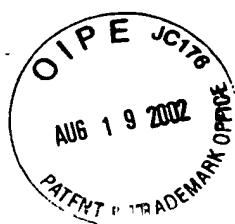
890 900 910 920  
 879 HDFHEIEGACKRGFQETLYVWNEPKWCIKGISLPEKKLAT SEQ ID 2  
 464 ----- SEC10

930 940 950 960  
 919 CETVDFWIKVGAGVGAFTAVLVALTCYFWKKNQKKKKTI SEQ ID 2  
 464 ----- SEC10

959 LNLFN  
 464 ----- SEC10

Decoration 'Decoration #1': Shade (with solid black) residues that match the consensus named 'Consensus #1' exactly.

FIG. 6B



	10	20	30	40
1	MLF RARG PVR GRG WGR PAAZAPR RGR SP PW SPA WIC C WALA			
1	-----	-----	-----	-----
	50	60	70	80
41	GCQAAWAGDLPSSSSRPLPPCQEKDYHFEYTECDSSGSRW			
1	-----	-----	-----	-----
	90	100	110	120
31	RVAIPNSAVD C SGL PDPV RGK ECT FSC AS G E Y L E	MKNQVC		
1	-----	-----	-----	-----
	130	140	150	160
121	SKCGEGTYSLGSGIKFDEWDELPAGESNIAATEMUTVVGPS			
7	SKCGEGTYSLGSGIKFDEWDELPAGESNIAATEMUTVVGPS			
	170	180	190	200
161	DSRPDGCNNSSWIPRGNYIESNRDCTVSLIYAVHLLKKSG			
47	DSRPDGCNNSSWIPRGNYIESNRDCTVSLIYAVHLLKKSG			
	210	220	230	240
201	YVPEEYQYVDNNTIFFEFPIQNDQCGEMDTTTDKWVKLTDN			
37	YVPEEYQYVDNNTIFFEFPIQNDQCGEMDTTTDKWVKLTDN			
	250	260	270	280
241	GEWGSHSVMLKSGTNILYWR TTGILMGSKAVKPVLVKNIT			
127	GEWGSHSVMLKSGTNILYWR TTGILMGSKAVKPVLVKNIT			
	290	300	310	320
281	IEGVAYTSECFCKPGTESNKGSPNCQVCPRNTYSEKGA			
167	IEGVAYTSECFCKPGTESNKGSPNCQVCPRNTYSEKGA			
	330	340	350	360
321	KECIRCKDDSQFES GSSECTERPPCTTKD YFQIHTPCDE			
207	KECIRCKDDSQFSEEGSSECTERPPCTTKD YFQIHTPCDE			
	370	380	390	400
359	EGKTQIMYKWI EPKICREDLTDAIRLPPSGEKKD C P P C N P			
247	EGKTQIMYKWI EPKICREDLTDAIRLPPSGEKKD C P P C N P			
	410	420	430	440
399	G F Y N N G S S C H F C P P G T F S D G T K E C R P C P A G T E P A L G F E Y			
287	G F Y N N G S S C H F C P P G T F S D G T K E C R P C P A G T E P A L G F E Y			
	450	460	470	480
439	KWWNVLPGNMKTSCFNVGNSKCDGMNGWEVAGDHIQSGAG			
327	KWWNVLPGNMKTSCFNVGNSKCDGMNGWEVAGDHIQSGAG			
	490	500	510	520
479	G S D N D Y L I L N L H I P G F K P P T S M T G A T G S E L G R I T F V F E T L			
367	G S D N D Y L I L N L H I P G F K P P T S M T G A T G S E L G R I T F V F E T L			

FIG. 7A



530 540 550 560  
 519 **CSADCVLIEFMVDINRKSTNVVESWGGTKEKQAYTHIEKKN** SEQ ID 4  
 407 **CSADCVLIEFMVDINRKSTNVVESWGGTKEKQAYTHIEKKN** SEC10

570 580 590 600  
 559 **A T E T F F T W A F Q R T N Q G Q D N R R F I N D M V K I Y S I T A T N A V D G V** SEQ ID 4  
 447 **A T E T F F T W G I P R E** SEC10

610 620 630 640  
 599 **A S S C R A C A L G S E Q S G S S C V P C P P G H Y I E K E T N Q C K E C P P D** SEQ ID 4  
 459 **- - - - -** SEC10

650 660 670 680  
 639 **T Y L S I H Q V Y G K E A C I P C G P G S K N N Q D H S V C Y S D C F F Y H E K** SEQ ID 4  
 459 **- - - - -** SEC10

690 700 710 720  
 679 **E N Q I L H Y D F S N L S S V G S L M N G P S F T S K G T K Y F H F F N I S L C** SEQ ID 4  
 459 **- - - - - L I Q G P** SEC10

730 740 750 760  
 719 **G H E G K K M A L C T N N I T D F T V K E I V A G S D D Y T N L V G A F V C Q S** SEQ ID 4  
 464 **- - - - -** SEC10

770 780 790 800  
 759 **T I I P S E S K G F R A A L S S Q S I I L A D T F I G V T V E T T L K N I N I K** SEQ ID 4  
 464 **- - - - -** SEC10

810 820 830 840  
 799 **E D M F P V P T S Q I P D V H F F Y K S S T A T T S C I N G R S T A V K M R C N** SEQ ID 4  
 464 **- - - - -** SEC10

850 860 870 880  
 839 **P T K S G A G V I S V P S K C P A G T C D G C T F Y F L W E S A E A C P L C T E** SEQ ID 4  
 464 **- - - - -** SEC10

890 900 910 920  
 879 **H D F H E I E G A C K R G F Q E T L Y V W N E P K W C I K G I S L P E K K L A T** SEQ ID 4  
 464 **- - - - -** SEC10

930 940 950 960  
 919 **C E T V D F W L K V G A G V G A F T A V L L V A L T C Y F W K K N Q K L E Y K Y** SEQ ID 4  
 464 **- - - - -** SEC10

970 980 990 1000  
 959 **S K L V M T T N S K E C E L P A A D S C A I M E G E D N E E E V V Y S N K Q S L** SEQ ID 4  
 464 **- - - - -** SEC10

1010 1020 1030  
 999 **L G K L K S L A T K E K E D H F E S V Q L K T S R S P N I .** SEQ ID 4  
 464 **- - - - - R** SEC10

Decoration 'Decoration #1': Shade (with solid black) residues that match the consensus named 'Consensus #1' exactly.

FIG. 7B

